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1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/017,479A

DATE: 07/16/2003

TIME: 15:45:40

Input Set : A:\13407-012001.txt

Output Set: N:\CRF4\07152003\J017479A.raw

4 <110> APPLICANT: Reenan, Robert A.
5 Rogina, Blanka
6 Helfand, Stephen L.
9 <120> TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING CELLULAR
10 TRANSPORTERS AND METHODS OF USE THEREOF
13 <130> FILE REFERENCE: 13407-012001
15 <140> CURRENT APPLICATION NUMBER: US 10/017,479A
16 <141> CURRENT FILING DATE: 2001-12-12
18 <150> PRIOR APPLICATION NUMBER: US 60/255,013
19 <151> PRIOR FILING DATE: 2000-12-12
21 <160> NUMBER OF SEQ ID NOS: 6
23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 1719
27 <212> TYPE: DNA
28 <213> ORGANISM: Drosophila melanogaster
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (1)...(1716)
34 <400> SEQUENCE: 1
35 atg gaa att gaa att ggc gaa caa ccc cag cct ccg gtg aag tgc tcc 48
36 Met Glu Ile Glu Ile Gly Glu Gln Pro Gln Pro Pro Val Lys Cys Ser
37 1 5 10 15
39 aac ttc ttc gct aac cac tgg aag gga ttg gtt gtg ttc ctg gtg ccg 96
40 Asn Phe Phe Ala Asn His Trp Lys Gly Leu Val Val Phe Leu Val Pro
41 20 25 30
43 ctg cta tgt ctg cct gtt atg ctg cta aac gaa ggc gcc gaa ttt ccg 144
44 Leu Leu Cys Leu Pro Val Met Leu Leu Asn Glu Gly Ala Glu Phe Arg
45 35 40 45
47 tgc atg tac ctc ctt ttg gta atg gcc ata ttt tgg gtt acg gaa gcc 192
48 Cys Met Tyr Leu Leu Val Met Ala Ile Phe Trp Val Thr Glu Ala
49 50 55 60
51 ttg cct ctc tat gtg acg tcc atg ata ccg att gtg gcc ttc cca ata 240
52 Leu Pro Leu Tyr Val Thr Ser Met Ile Pro Ile Val Ala Phe Pro Ile
53 65 70 75 80
55 atg ggt ata atg agc tcg gat cag act tgc cgc ttg tac ttc aag gat 288
56 Met Gly Ile Met Ser Ser Asp Gln Thr Cys Arg Leu Tyr Phe Lys Asp
57 85 90 95
59 acg ctg gtg atg ttc atg ggc ggc att atg gtc gcc ctg gct gtg gag 336
60 Thr Leu Val Met Phe Met Gly Gly Ile Met Val Ala Leu Ala Val Glu
61 100 105 110
63 tac tgt aat cta cac aaa cgt ctt gcc ttg agg gta atc cag atc gtg
64 Tyr Cys Asn Leu His Lys Arg Leu Ala Leu Arg Val Ile Gln Ile Val

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65	115	120	125	
67	ggc tgc agt ccc cgc aga tta cac ttt ggc ctc atc atg gtt aca atg			432
68	Gly Cys Ser Pro Arg Arg Leu His Phe Gly Leu Ile Met Val Thr Met			
69	130	135	140	
71	ttt ttg agc atg tgg att tcg aac gcc gcc tgt act gcc atg atg tgt			480
72	Phe Leu Ser Met Trp Ile Ser Asn Ala Ala Cys Thr Ala Met Met Cys			
73	145	150	155	160
75	ccg att atc caa gcc gtg ctg gag gag ctg cag gct cag ggt gtc tgc			528
76	Pro Ile Ile Gln Ala Val Leu Glu Glu Leu Gln Ala Gln Gly Val Cys			
77	165	170	175	
79	aaa atc aac cat gag cct caa tac caa atc gtt gga ggc aac aag aaa			576
80	Lys Ile Asn His Glu Pro Gln Tyr Gln Ile Val Gly Gly Asn Lys Lys			
81	180	185	190	
83	aac aac gag gat gag cca cca tac ccc acc aag atc act ctg tgc tac			624
84	Asn Asn Glu Asp Glu Pro Pro Tyr Pro Thr Lys Ile Thr Leu Cys Tyr			
85	195	200	205	
87	tat ctg ggc att gcc tac gcc tcc tcg ctg ggt ggc tgt gga acc atc			672
88	Tyr Leu Gly Ile Ala Tyr Ala Ser Ser Leu Gly Gly Cys Gly Thr Ile			
89	210	215	220	
91	atc gga act gcc acc aat ctt acc ttc aag ggc atc tac gag gct cgt			720
92	Ile Gly Thr Ala Thr Asn Leu Thr Phe Lys Gly Ile Tyr Glu Ala Arg			
93	225	230	235	240
95	ttc aag aac tcc acc gaa cag atg gac ttc ccc acc ttc atg ttc tac			768
96	Phe Lys Asn Ser Thr Glu Gln Met Asp Phe Pro Thr Phe Met Phe Tyr			
97	245	250	255	
99	tcg gtg cca tcc atg ttg gtc tac acc ttg ctg aca ttc gtg ttc ctg			816
100	Ser Val Pro Ser Met Leu Val Tyr Thr Leu Leu Thr Phe Val Phe Leu			
101	260	265	270	
103	caa tgg cac ttc atg ggt ctg tgg cgt ccc aag agc aag gag gca cag			864
104	Gln Trp His Phe Met Gly Leu Trp Arg Pro Lys Ser Lys Glu Ala Gln			
105	275	280	285	
107	gaa gtc cag agg gga cga gag ggc gat gtc gcc aaa aag gtt atc			912
108	Glu Val Gln Arg Gly Arg Glu Gly Ala Asp Val Ala Lys Lys Val Ile			
109	290	295	300	
111	gat cag cgc tac aag gat ctg ggt ccc atg tcc att cac gag atc caa			960
112	Asp Gln Arg Tyr Lys Asp Leu Gly Pro Met Ser Ile His Glu Ile Gln			
113	305	310	315	320
115	gtg atg att ctg ttc att ttt atg gtt gtg atg tac ttc acc cgc aag			1008
116	Val Met Ile Leu Phe Ile Phe Met Val Val Met Tyr Phe Thr Arg Lys			
117	325	330	335	
119	ccc ggc atc ttt ttg gga tgg gcc gat ttg ctg aat tcc aag gac att			1056
120	Pro Gly Ile Phe Leu Gly Trp Ala Asp Leu Leu Asn Ser Lys Asp Ile			
121	340	345	350	
123	cgt aac tct atg ccc act att ttt gtc gtc gtc atg tgc ttc atg ctg			1104
124	Arg Asn Ser Met Pro Thr Ile Phe Val Val Val Met Cys Phe Met Leu			
125	355	360	365	
127	ccc gcc aat tat gct ttc cta cgc tac tgc acc aag aga cgc ggt ggt cca			1152
128	Pro Ala Asn Tyr Ala Phe Leu Arg Tyr Cys Thr Arg Arg Gly Gly Pro			
129	370	375	380	

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131	gtg	ccc	acg	ggt	ccc	act	cca	tcg	ctg	atc	acc	tgg	aag	ttc	atc	cag	1200
132	Val	Pro	Thr	Gly	Pro	Thr	Pro	Ser	Leu	Ile	Thr	Trp	Lys	Phe	Ile	Gln	
133	385				390					395						400	
135	acc	aag	gtg	cca	tgg	ggt	ctg	gtg	ttc	ctg	ctt	ggc	ggt	ggc	ttc	gct	1248
136	Thr	Lys	Val	Pro	Trp	Gly	Leu	Val	Phe	Leu	Leu	Gly	Gly	Phe	Ala		
137							405			410						415	
139	ttg	gcc	gaa	ggc	agc	aag	cag	agc	ggc	atg	gcc	aag	ctg	att	ggc	aat	1296
140	Leu	Ala	Glu	Gly	Ser	Lys	Gln	Ser	Gly	Met	Ala	Lys	Leu	Ile	Gly	Asn	
141					420					425						430	
143	gct	ctg	att	gga	ttg	aag	gtt	ctg	ccc	aac	tct	gtc	ctc	tta	ctg	gtg	1344
144	Ala	Leu	Ile	Gly	Leu	Lys	Val	Leu	Pro	Asn	Ser	Val	Leu	Leu	Leu	Val	
145							435			440						445	
147	gtc	atc	ctg	gtg	gct	gtg	ttc	ctg	acc	gcc	ttc	agc	tcc	aat	gtg	gcg	1392
148	Val	Ile	Leu	Val	Ala	Val	Phe	Leu	Thr	Ala	Phe	Ser	Ser	Asn	Val	Ala	
149					450					455						460	
151	att	gcc	aac	att	att	att	ccc	gtt	ctg	gcc	gag	atg	tcc	ctg	gcc	att	1440
152	Ile	Ala	Asn	Ile	Ile	Ile	Pro	Val	Leu	Ala	Glu	Met	Ser	Leu	Ala	Ile	
153					465					470						480	
155	gag	atc	cat	cct	ctg	tac	ctg	atc	ctg	ccc	gct	ggc	ttg	gcc	tgc	agt	1488
156	Glu	Ile	His	Pro	Leu	Tyr	Leu	Ile	Leu	Pro	Ala	Gly	Leu	Ala	Cys	Ser	
157							485			490						495	
159	atg	gcc	ttc	cac	ctg	ccg	gtt	agt	act	ccg	ccc	aac	gct	ttg	gtt	gct	1536
160	Met	Ala	Phe	His	Leu	Pro	Val	Ser	Thr	Pro	Pro	Asn	Ala	Leu	Val	Ala	
161					500					505						510	
163	ggc	tat	gcc	aac	att	agg	acg	aag	gac	atg	gcc	att	gct	gga	atc	ggt	1584
164	Gly	Tyr	Ala	Asn	Ile	Arg	Thr	Lys	Asp	Met	Ala	Ile	Ala	Gly	Ile	Gly	
165					515					520						525	
167	ccg	acc	atc	att	acc	atc	acc	ctg	ttt	gtt	ttc	tgc	caa	acc	tgg		1632
168	Pro	Thr	Ile	Ile	Thr	Ile	Ile	Thr	Leu	Phe	Val	Phe	Cys	Gln	Thr	Trp	
169					530					535						540	
171	ggc	ctg	gtt	gtc	tat	ccg	aac	ctt	aac	tcg	ttc	ccc	gaa	tgg	gct	cag	1680
172	Gly	Leu	Val	Val	Tyr	Pro	Asn	Leu	Asn	Ser	Phe	Pro	Glu	Trp	Ala	Gln	
173					545					550						560	
175	att	tat	gcc	gct	gca	gca	ctg	gga	aac	aag	acg	cac	tag				1719
176	Ile	Tyr	Ala	Ala	Ala	Ala	Leu	Gly	Asn	Lys	Thr	His					
177							565			570							
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181	<211>	LENGTH:	572														
182	<212>	TYPE:	PRT														
183	<213>	ORGANISM:	Drosophila	melanogaster													
185	<400>	SEQUENCE:	2														
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187	1				5				10					15			
188	Asn	Phe	Phe	Ala	Asn	His	Trp	Lys	Gly	Leu	Val	Val	Phe	Leu	Val	Pro	
189					20				25					30			
190	Leu	Leu	Cys	Leu	Pro	Val	Met	Leu	Leu	Asn	Glu	Gly	Ala	Glu	Phe	Arg	
191					35				40					45			
192	Cys	Met	Tyr	Leu	Leu	Leu	Val	Met	Ala	Ile	Phe	Trp	Val	Thr	Glu	Ala	
193					50				55					60			

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194 Leu Pro Leu Tyr Val Thr Ser Met Ile Pro Ile Val Ala Phe Pro Ile
 195 65 70 75 80
 196 Met Gly Ile Met Ser Ser Asp Gln Thr Cys Arg Leu Tyr Phe Lys Asp
 197 85 90 95
 198 Thr Leu Val Met Phe Met Gly Gly Ile Met Val Ala Leu Ala Val Glu
 199 100 105 110
 200 Tyr Cys Asn Leu His Lys Arg Leu Ala Leu Arg Val Ile Gln Ile Val
 201 115 120 125
 202 Gly Cys Ser Pro Arg Arg Leu His Phe Gly Leu Ile Met Val Thr Met
 203 130 135 140
 204 Phe Leu Ser Met Trp Ile Ser Asn Ala Ala Cys Thr Ala Met Met Cys
 205 145 150 155 160
 206 Pro Ile Ile Gln Ala Val Leu Glu Glu Leu Gln Ala Gln Gly Val Cys
 207 165 170 175
 208 Lys Ile Asn His Glu Pro Gln Tyr Gln Ile Val Gly Gly Asn Lys Lys
 209 180 185 190
 210 Asn Asn Glu Asp Glu Pro Pro Tyr Pro Thr Lys Ile Thr Leu Cys Tyr
 211 195 200 205
 212 Tyr Leu Gly Ile Ala Tyr Ala Ser Ser Leu Gly Gly Cys Gly Thr Ile
 213 210 215 220
 214 Ile Gly Thr Ala Thr Asn Leu Thr Phe Lys Gly Ile Tyr Glu Ala Arg
 215 225 230 235 240
 216 Phe Lys Asn Ser Thr Glu Gln Met Asp Phe Pro Thr Phe Met Phe Tyr
 217 245 250 255
 218 Ser Val Pro Ser Met Leu Val Tyr Thr Leu Leu Thr Phe Val Phe Leu
 219 260 265 270
 220 Gln Trp His Phe Met Gly Leu Trp Arg Pro Lys Ser Lys Glu Ala Gln
 221 275 280 285
 222 Glu Val Gln Arg Gly Arg Glu Gly Ala Asp Val Ala Lys Lys Val Ile
 223 290 295 300
 224 Asp Gln Arg Tyr Lys Asp Leu Gly Pro Met Ser Ile His Glu Ile Gln
 225 305 310 315 320
 226 Val Met Ile Leu Phe Ile Phe Met Val Val Met Tyr Phe Thr Arg Lys
 227 325 330 335
 228 Pro Gly Ile Phe Leu Gly Trp Ala Asp Leu Leu Asn Ser Lys Asp Ile
 229 340 345 350
 230 Arg Asn Ser Met Pro Thr Ile Phe Val Val Val Met Cys Phe Met Leu
 231 355 360 365
 232 Pro Ala Asn Tyr Ala Phe Leu Arg Tyr Cys Thr Arg Arg Gly Gly Pro
 233 370 375 380
 234 Val Pro Thr Gly Pro Thr Pro Ser Leu Ile Thr Trp Lys Phe Ile Gln
 235 385 390 395 400
 236 Thr Lys Val Pro Trp Gly Leu Val Phe Leu Leu Gly Gly Phe Ala
 237 405 410 415
 238 Leu Ala Glu Gly Ser Lys Gln Ser Gly Met Ala Lys Leu Ile Gly Asn
 239 420 425 430
 240 Ala Leu Ile Gly Leu Lys Val Leu Pro Asn Ser Val Leu Leu Leu Val
 241 435 440 445
 242 Val Ile Leu Val Ala Val Phe Leu Thr Ala Phe Ser Ser Asn Val Ala

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243 450 455 460
 244 Ile Ala Asn Ile Ile Ile Pro Val Leu Ala Glu Met Ser Leu Ala Ile
 245 465 470 475 480
 246 Glu Ile His Pro Leu Tyr Leu Ile Leu Pro Ala Gly Leu Ala Cys Ser
 247 485 490 495
 248 Met Ala Phe His Leu Pro Val Ser Thr Pro Pro Asn Ala Leu Val Ala
 249 500 505 510
 250 Gly Tyr Ala Asn Ile Arg Thr Lys Asp Met Ala Ile Ala Gly Ile Gly
 251 515 520 525
 252 Pro Thr Ile Ile Thr Ile Ile Thr Leu Phe Val Phe Cys Gln Thr Trp
 253 530 535 540
 254 Gly Leu Val Val Tyr Pro Asn Leu Asn Ser Phe Pro Glu Trp Ala Gln
 255 545 550 555 560
 256 Ile Tyr Ala Ala Ala Leu Gly Asn Lys Thr His
 257 565 570
 259 <210> SEQ ID NO: 3
 260 <211> LENGTH: 562
 261 <212> TYPE: PRT
 262 <213> ORGANISM: Drosophila melanogaster
 264 <400> SEQUENCE: 3
 265 Met Ala Glu Pro Gly Glu Gln Arg Lys Phe Val Leu Gly Arg Cys Cys
 266 1 5 10 15
 267 Ile Phe His Trp Arg Gly Lys Ala Ser Ile Ile Ile Pro Leu Ile Thr
 268 20 25 30
 269 Leu Pro Ile Leu Ile Tyr Gly Phe Gln Thr Asp Met Ala Glu Phe Lys
 270 35 40 45
 271 Cys Leu Trp Leu Ile Val Thr Met Ala Leu Leu Trp Ile Thr Glu Thr
 272 50 55 60
 273 Leu Pro Ile Tyr Val Thr Ala Leu Phe Pro Leu Val Phe Cys Pro Leu
 274 65 70 75 80
 275 Leu Gly Leu Val Asn Ala Ser Ile Val Cys Lys Gln Tyr Phe Thr Asp
 276 85 90 95
 277 Thr Ile Val Val Phe Leu Gly Gly Leu Ile Val Ala Leu Gly Ile Glu
 278 100 105 110
 279 Tyr Ser Asn Leu His Thr Arg Ile Ala Leu Arg Val Ile Arg Ile Val
 280 115 120 125
 281 Gly Gly Ser Pro Arg Arg Leu Phe Val Gly Leu Met Ser Val Ser Thr
 282 130 135 140
 283 Phe Met Gly Leu Trp Ile Ser Asn Ser Ala Gly Thr Ala Met Met Cys
 284 145 150 155 160
 285 Pro Ile Val Lys Ala Leu Val Asn Glu Leu Asp Thr Asn Lys Ile Phe
 286 165 170 175
 287 Pro Val Tyr Met Thr Gln Glu Glu Pro Val Glu Glu Gly Glu Pro
 288 180 185 190
 289 Pro His Pro Ser Lys Ile Thr Val Ala Phe Tyr Ala Gly Ile Ala Tyr
 290 195 200 205
 291 Ala Ser Ser Ile Gly Gly Leu Gly Thr Leu Ile Gly Thr Gly Thr Asn
 292 210 215 220
 293 Leu Val Phe Arg Gly Ile Tyr Thr Glu Arg Phe Pro Thr Ser Thr Val

VERIFICATION SUMMARY

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